

CC inhibition of fertility. The present sequence represents the human sperm
CC specific surface protein C58
XX
SQ Sequence 124 AA;

Query Match 100.0%; Score 684; DB 4; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLCTLLLVMLPFGTGVKDCVFCGLTDSMOCPEGTYMHCGDDECFTHGVAPEGVPV 60
DB 1 MVLCTLLLVMLPFGTGVKDCVFCGLTDSMOCPEGTYMHCGDDECFTHGVAPEGVPV 60
QY 61 INKGLRATSCGLEBPVSRYGVYISLTNNCTGRLCNRAPSSQTVGATTSIALGLGMLLP 120
DB 61 INKGLRATSCGLEBPVSRYGVYISLTNNCTGRLCNRAPSSQTVGATTSIALGLGMLLP 120
QY 121 PRL 124
DB 121 PRL 124

RESULT 2

AA089146 ID AAG89146 standard; protein; 124 AA.

XX AC AAG89146;

XX DT 11-SEP-2001 (first entry)

XX DE Human secreted protein, SEQ ID NO: 266.

XX DE Human secreted protein; gene therapy; vaccine; treatment; diagnosis;

KW GENSET.

XX OS Homo sapiens.

XX PN MO200142451-A2.

XX PD 14-JUN-2001.

XX PF 07-DEC-2000; 2000MO-IB001938.

XX PR 08-DEC-1999; 99US-0169629P.

XX PR 06-MAR-2000; 2000US-0187470P.

XX (GENSET) GENSET.

XX PI Dumas Milne Edwards J, Bougueleret L, Jcbert S;

XX DR WPI; 2001-367870/38.

XX DR N-PSDB; AAH64749.

XX PT Full length GENSET human nucleic acids encoding potentially secreted
XX PT proteins, useful in gene therapy and vaccination against a variety of
XX PT diseases, and for diagnosis of those diseases.

XX PS Claim 21; Page 807; 921pp; English.

XX CC The invention relates to full length GENSET human nucleic acids encoding
XX CC potentially secreted proteins. The nucleic acids and the polypeptides
XX CC they encode may be used in the prevention, treatment and diagnosis of
XX CC diseases associated with inappropriate GENSET gene expression. For
XX CC example, they be used to treat disorders associated with decreased GENSET
XX CC gene expression by rectifying mutations or deletions in a patient's
XX CC genome that affect the activity of GENSET or by supplementing the
XX CC patient's own production of GENSET polypeptides. Conversely, antisense
XX CC nucleic acid molecules may be administered to down regulate GENSET
XX CC expression by binding with the cells' own genes and preventing their
XX CC expression. The sense and antisense nucleic acids may also be used as DNA
XX CC probes in diagnostic assays to detect and quantitate the presence of
XX CC similar nucleic acid sequences in samples, and hence to determine which
XX CC patients may be in need of restorative therapy. The GENSET polypeptides

CC may be used as antigens in the production of antibodies and in assays to
CC identify modulators (agonists and antagonists) of GENSET polypeptide
CC expression and activity. The present sequence is a GENSET polypeptide of
CC the invention
XX

SQ Sequence 124 AA;

Query Match 100.0%; Score 684; DB 4; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLCTLLLVMLPFGTGVKDCVFCGLTDSMOCPEGTYMHCGDDECFTHGVAPEGVPV 60
DB 1 MVLCTLLLVMLPFGTGVKDCVFCGLTDSMOCPEGTYMHCGDDECFTHGVAPEGVPV 60
QY 61 INKGLRATSCGLEBPVSRYGVYISLTNNCTGRLCNRAPSSQTVGATTSIALGLGMLLP 120
DB 61 INKGLRATSCGLEBPVSRYGVYISLTNNCTGRLCNRAPSSQTVGATTSIALGLGMLLP 120
QY 121 PRL 124
DB 121 PRL 124

RESULT 3

AA083605 ID AA083605 standard; protein; 124 AA.

XX AC AA083605;

XX DT 08-MAY-2002 (first entry)

XX DE Human PRO protein, Seq ID No 28.

XX DE Human; secreted protein; PRO; tumour; lung cancer; colon cancer;

KW breast cancer; prostate tumour; rectal tumour; liver tumour;

KW pericyte cell proliferation; chondrocyte cell proliferation;

XX KW tumour necrosis factor-alpha.

XX OS Homo sapiens.

XX PN MO200208288-A2.

XX PD 31-JAN-2002.

XX PF 29-JUN-2001; 2001MO-US021066.

XX PR 20-JUL-2000; 2000US-0219556P.

XX PR 25-JUL-2000; 2000US-0220585P.

XX PR 25-JUL-2000; 2000US-0220605P.

XX PR 25-JUL-2000; 2000US-0220607P.

XX PR 25-JUL-2000; 2000US-0220624P.

XX PR 25-JUL-2000; 2000US-0220638P.

XX PR 25-JUL-2000; 2000US-0220664P.

XX PR 25-JUL-2000; 2000US-0220666P.

XX PR 26-JUL-2000; 2000US-0220893P.

XX PR 28-JUL-2000; 2000MO-US020710.

XX PR 28-AUG-2000; 2000US-0222425P.

XX PR 22-AUG-2000; 2000US-0227133P.

XX PR 23-AUG-2000; 2000MO-US023522.

XX PR 24-AUG-2000; 2000MO-US023528.

XX PR 10-NOV-2000; 2000MO-US030873.

XX PR 28-NOV-2000; 2000US-0253646P.

XX PR 01-DEC-2000; 2000MO-US032678.

XX PR 20-DEC-2000; 2000US-00747259.

XX PR 20-DEC-2000; 2000MO-US034956.

XX PR 28-FEB-2001; 2001MO-US006520.

XX PR 01-MAR-2001; 2001MO-US006666.

XX PR 22-MAR-2001; 2001US-00816744.

XX PR 10-MAY-2001; 2001US-00854208.

XX PR 10-MAY-2001; 2001US-00854280.

XX PR 25-MAY-2001; 2001MO-US017092.

XX

PA (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX WPI; 2002-172001/22.
 DR N-PSDB; ABRK35549.
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumors such
 PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
 PT or liver tumor.
 XX
 XX Claim 11; Fig 28; 359pp; English.
 XX The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumors, especially lung
 CC cancer, colon cancer, breast tumor, prostate tumor, rectal tumor or
 CC liver tumor. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumor necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
 CC protein sequences of the invention
 XX
 SO Sequence 124 AA;
 Query Match 100.0%; Score 684; DB 5; Length 124;
 Best Local Similarity 100.0%; Pred. No. 2.3e-54;
 Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MVLQWLLLVLMALPPTGVKDCVFCELTDSMOCPECTVHCGDEDCFTGHGAPETGV 60
 DB 1 MVLQWLLLVLMALPPTGVKDCVFCELTDSMOCPECTVHCGDEDCFTGHGAPETGV 60
 QY 61 INKGCIRATSCGLEBPVSRYGVYSLTTCCTGRLCNRAPSSQTVGATTSIALGLMLP 120
 DB 61 INKGCIRATSCGLEBPVSRYGVYSLTTCCTGRLCNRAPSSQTVGATTSIALGLMLP 120
 QY 121 PRL 124
 DB 121 PRL 124
 QY 121 PRL 124
 DB 121 PRL 124
 RESULT 4
 AAEL17451 standard; protein; 124 AA.
 AC AAEL17451;
 DT 22-APR-2002 (first entry)
 DE Human secreted protein, zuparl.
 DE Human secreted protein, zuparl.
 KW tissue; secreted protein; zuparl; inflammation; immunosuppressive; cancer;
 KW fibrosis; remodelling; vaccine; autoimmune disease; cell-mediated immunity;
 KW fibrinolysis; coagulation; circulatory anomaly; wound healing; vulnary;
 KW contraception; sperm motility; fertilisation; immunoc contraceptive;
 KW spermatogenesis; antiinflammatory; contraceptive; antiinfertility;
 KW gene therapy; chromosome 19q.13.32.
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..19
 FT /label= signal_peptide

FT Protein 20..124
 FT /label= Mature_human_zuparl_protein
 FT Domain 20..110
 FT /note= "Extracellular domain"
 FT Region 22..24
 FT /note= "Beta strand"
 FT Disulfide-bond 23..47
 FT Disulfide-bond 25..34
 FT Region 38..40
 FT /note= "Beta strand"
 FT Disulfide-bond 41..65
 FT Region 46..52
 FT /note= "Beta strand"
 FT Region 60..66
 FT /note= "Beta strand"
 FT Disulfide-bond 71..90
 FT Region 76..80
 FT /note= "Alpha helix"
 FT Region 89..91
 FT /note= "Beta strand"
 FT Disulfide-bond 91..95
 FT Domain 111..124
 FT /note= "Membrane associated domain"
 XX
 XX WO200202636-A2.
 XX 10-JAN-2002.
 XX
 XX 02-JUL-2001; 2001WO-US021167.
 XX
 XX 30-JUN-2000; 2000US-0215446P.
 XX
 XX (ZYMO) ZYMOGENETICS INC.
 XX
 XX Shepard PO, Bishop PD, Presnell SR, Gilbert T;
 XX WPI; 2002-154734/20.
 XX N-PSDB; AAD28085.
 XX
 XX Novel zuparl polypeptide useful for reducing inflammation, enhancing
 PT viability of cryopreserved sperm, sperm motility, egg-sperm interactions,
 PT and fertilization, or as components in antiinfertility vaccines.
 PT
 PS Claim 1; Page 2; 94pp; English.
 XX The present invention relates to a novel human secreted protein
 CC designated zuparl and its nucleic acid. zuparl gene is used in gene
 CC therapy and is located on chromosome 19q.13.32. Zuparl is useful in
 CC competing with complement or other membrane targeted complexes in
 CC reducing inflammation, coagulation or tissue remodeling and for treating
 CC autoimmune diseases, circulatory anomalies and blocking tissue remodeling
 CC in aggressive cancers, and used in wound healing. Zuparl is used in
 CC applications related to fibrinolysis coagulation, remodeling wound
 CC healing, contraception and fertility. Zuparl are useful in enhancing
 CC viability of cryopreserved sperm, as a component in acrosome reaction,
 CC enhancing sperm motility and enhancing egg-sperm interactions and is
 CC useful for enhancing fertilisation during assisted reproduction in humans
 CC and in animals by preventing attack by complement. In cases where
 CC pregnancy is not desired, zuparl may function as germ-cell-specific
 CC antigens for use as components in immunocontraceptive or anti-fertility
 CC vaccines to induce formation of antibodies to selectively inhibit a cell-
 CC mediated immunity. Zuparl are useful as markers for testis tissue or
 CC sperm and as components of defined cell culture media to replace serum.
 CC Zuparl blocking antibodies can also be used to target zuparl on specific
 CC cell populations, inactivating zuparl and rendering the cells susceptible
 CC to lysis by the complement system. Zuparl antibodies could also act as
 CC antagonists by inhibiting components of spermatogenesis and/or sperm
 CC activation and used for contraception in domestic animals and livestock.
 CC The present sequence is human zuparl protein
 XX
 SO Sequence 124 AA;
 Query Match 100.0%; Score 684; DB 5; Length 124;

	Best Local Similarity	100.0%	Pred. No. 2,3e-54						
	Matches	124	Conservative	0	Mismatches	0	Indels	0	Gaps
QY	1	MVLCLMLLLVNALP	PGITGVKD	CVFC	ELTDSMOC	PGTYMH	CGDDEDC	FTGHGVA	PGTGPV 60
Db	1	MVLCLMLLLVNALP	PGITGVKD	CVFC	ELTDSMOC	PGTYMH	CGDDEDC	FTGHGVA	PGTGPV 60
QY	61	INKCCLNATSCGLE	EPVSYRGV	TSLLTN	CCTGRLCN	RAPSSQ	TVGATTSL	ALGIMLLP 120	
Db	61	INKCCLNATSCGLE	EPVSYRGV	TSLLTN	CCTGRLCN	RAPSSQ	TVGATTSL	ALGIMLLP 120	
QY	121	PRL	124						
Db	121	PRL	124						

	Query Match	100.0%	Score 684	DB 5	Length 124	
	Best Local Similarity	100.0%	Pred. No. 2,3e-54			
	Matches 124	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	1	MVLQMLLLLVWALPFGTTGVND	CVFCELTDSMOC	PGTYMHCGDDEDC	FTGHGVAFGTGPV	60
Db	1	MVLQMLLLLVWALPFGTTGVND	CVFCELTDSMOC	PGTYMHCGDDEDC	FTGHGVAFGTGPV	60
QY	61	INKGCLRATSCGLEBPVS	YRGVYTSLLTNCCTG	ALCNRAPESSQVYGATT	SLALGIMLLP	120
Db	61	INKGCLRATSCGLEBPVS	YRGVYTSLLTNCCTG	ALCNRAPESSQVYGATT	SLALGIMLLP	120
QY	121	PRLL	124			
Db	121	PRLL	124			

XX	RESULT 5
XX	AAU83232
ID	AAU83232 standard; protein; 124 AA.
AC	AAU83232;
XX	
DT	08-MAY-2002 (first entry)
XX	
DE	Novel secreted protein Z9J1828G2P.
XX	
KW	Protein secretion; mammalian secreted polypeptide; MSP.
OS	Homo sapiens.
XX	
PN	W0200202621-A2.
XX	
PD	10-JAN-2002.
XX	
PF	28-JUN-2001; 2001KO-US020638.
XX	
PR	30-JUN-2000; 2000US-0215446P.
XX	
PA	(ZYMO) ZYMOGENETICS INC.
XX	
PI	Shepard PO, Presnell SR;
XX	
DR	WPI; 2002-147999/19.
DR	N-PSDB; ABK3147.
PT	Novel isolated mammalian secreted polypeptide useful in therapeutic and
PT	diagnostic methods, to direct secretion of other proteins of interest
PT	from host cell, as educational tools, and as laboratory practicum kits.
XX	
PS	Claim 12; Page 382-383; 397p; English.
XX	
CC	The invention describes an isolated mammalian secreted polypeptide (MSP)
CC	(1). (I) is useful to direct the secretion of other proteins of interest
CC	from a host cell, to monitor secretion of proteins, to degenerate
CC	sequences comprising all nucleotide sequences encoding a particular
CC	polypeptide, to screen for cell metabolism effecting receptors, for
CC	identifying new target receptors and drug design, for identifying, for
CC	protein purification, for determining the weight of expressed MSP
CC	polypeptides as a ratio to total protein expressed, for identifying
CC	peptide cleavage sites, for coupling amino and carboxy terminal tags, for
CC	amino acid sequence analysis, for monitoring biological activities of the
CC	protein in vitro and in vivo, and to teach analytical skills and as
CC	reagents for the study of cells, receptors, and other binding molecules.
CC	The polynucleotide is useful for radiation hybrid mapping, and somatic
CC	cell genetic technique developed for constructing high-resolution,
CC	continuous maps of mammalian chromosomes. Reagents disclosed in the
CC	invention may be used to detect metabolic abnormalities characterised by
CC	over or under production of the protein. This is the amino acid sequence
CC	of a mammalian secreted polypeptide, described in the method of the
XX	invention
XX	
XQ	Sequence 124 AA;

XX	ABU80752 standard; protein; 124 AA.
ID	ABU80752
AC	ABU80752;
XX	
DT	23-JUN-2003 (first entry)
XX	
DE	Human PRO polypeptide #14.
XX	
KW	Human; PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
XX	
OS	Homo sapiens.
PN	US2003036635-A1.
PD	20-FEB-2003.
PF	28-AUG-2002; 2002US-00230163.
XX	
PR	25-JUL-2000; 2000US-0220638P. 01-JUN-2001; 2001WO-US017800. 29-JUN-2001; 2001WO-US021066. 09-APR-2002; 2002US-00119480.
XX	
PI	(GETH) GENENTECH INC.
PA	Baker KD, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ; Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI; WPI; 2003-342045/32.
DR	N-PDSB; ACA66854.
PT	One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating tumor.
PS	Claim 11; Fig 28; 314pp; English.
CC	The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. ABU80739-ABU80860 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/patseq/DIDentry.html
SO	Sequence 124 AA;
Query Match	100.0%; Score 684; DB 6; Length 124;
Best Local Similarity	100.0%; Pred. No. 2,3e-54;

Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLCMILLVMAIPPTGTGKDCVFCCLTDSMQCPGTVMHCGDDEDCFTGHGVAPEGTPV 60
DB 1 MYLCMILLVMAIPPTGTGKDCVFCCLTDSMQCPGTVMHCGDDEDCFTGHGVAPEGTPV 60

QY 61 INKGLRATSCGLEBVSRYGVVYSLTNNCTGRLCNRA PSSQTGATTSIALGLMLLP 120
DB 61 INKGLRATSCGLEBVSRYGVVYSLTNNCTGRLCNRA PSSQTGATTSIALGLMLLP 120

QY 121 PRL 124
DB 121 PRL 124

RESULT 7
ABO33718
ID ABO33718 standard; protein; 124 AA.
XX
AC ABO33718;
XX
DT 17-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO9862.
XX
KW Human; secreted and transmembrane protein; PRO; cytosolic;
KW antirhectic; osteopathic; gene therapy; TNF-Agonist-Alpha;
KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
KW pharmaceutical; diagnostic; biosensor; bioindicator; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; bone disorder; cartilage disorder; sports injury;
KW arthritis; wound.

OS Homo sapiens.
XX
PN US2003045687-A1.
XX
PD 06-MAR-2003.
XX
PF 12-AUG-2002; 2002US-00218631.
XX
PR 01-JUN-2001; 2001WO-US017800.
XX
PR 29-JUN-2001; 2001WO-US021066.
XX
PR 09-APR-2002; 2002US-00119480.
XX
PA (GENTH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-512315/48.
XX
DR N-PSDB; ACDB8606.
XX
PT New genes, and its encoded secreted and transmembrane polypeptides,
XX useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
XX pericyte proliferation, especially for treating lung tumors, arthritis or
XX wounds in a mammal.

Claim 11; Fig 28; 314P; English.

The invention describes an isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
CC fully defined in the specification; or (b) any of 122 nucleotide
CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
CC specification; or the full length coding sequence of any these 122
CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC particularly useful for detecting tumors (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of TNF-alpha from human blood,
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells, for stimulating proliferation of pericyte cells, or for modulating

CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
CC polypeptide is also useful for treating tumors or various bone and/or
CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridization probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide

Sequence 124 AA;

Query Match 100.0%; Score 684; DB 6; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLCMILLVMAIPPTGTGKDCVFCCLTDSMQCPGTVMHCGDDEDCFTGHGVAPEGTPV 60
DB 1 MYLCMILLVMAIPPTGTGKDCVFCCLTDSMQCPGTVMHCGDDEDCFTGHGVAPEGTPV 60

QY 61 INKGLRATSCGLEBVSRYGVVYSLTNNCTGRLCNRA PSSQTGATTSIALGLMLLP 120
DB 61 INKGLRATSCGLEBVSRYGVVYSLTNNCTGRLCNRA PSSQTGATTSIALGLMLLP 120

QY 121 PRL 124
DB 121 PRL 124

RESULT 8
ABU82061
ID ABU82061 standard; protein; 124 AA.
XX
AC ABU82061;
XX
DT 25-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO9862.
XX
KW Human; secreted and transmembrane protein; PRO; cardiac; cytosolic;
KW antiangiogenic; hypotensive; vulnery; antiarteriosclerotic;
KW gene therapy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; cardiac hypertrophy; cirrhosis; cancer;
KW age-related macular degeneration; atherosclerosis; hypertension;
KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
KW liver carcinoma; wound healing; chromosome mapping; gene mapping.

OS Homo sapiens.
XX
PN US2003088063-A1.
XX
PD 08-MAY-2003.
XX
PF 12-AUG-2002; 2002US-00219003.
XX
PR 25-JUL-2000; 2000US-0220664P.
XX
PR 01-JUN-2001; 2001WO-US017800.
XX
PR 29-JUN-2001; 2001WO-US021066.
XX
PR 09-APR-2002; 2002US-00119480.
XX
PA (GENTH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-393229/37.
XX
DR N-PSDB; ACA68510.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PS infarction), endothelial or angiogenic disorders in a mammal.
XX
XX
PS Claim 11; Fig 28; 314pp; English.
XX
CC The invention describes one hundred and eighty seven nucleic acids
CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
CC treating or diagnosing a cardiovascular, endothelial or angiogenic
CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
CC related macular degeneration, atherosclerosis, hypertension, arterial
CC stenosis, rheumatoid arthritis, angina, myocardial infarctions,
CC thromboplethitis, lymphangitis, tumour angiogenesis (such as breast
CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
CC have applications in molecular biology, including use as hybridisation
CC probes, and in chromosome and gene mapping. This is the amino acid
CC sequence of a novel human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 124 AA;
XX
Query Match 100.0%; Score 684; DB 6; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MVLQWLLILVMAIPGTTGVKDCVFCBLTDSMOCPEYMHCGDDEDCFTGHGVAPEGTPV 60
DB 1 MVLQWLLILVMAIPGTTGVKDCVFCBLTDSMOCPEYMHCGDDEDCFTGHGVAPEGTPV 60
QY 61 INKGCLRATSCGLEBPVSRYGVYSLTTNCTGRLCNRAPSSQTVGATTSIALGLMLLP 120
DB 61 INKGCLRATSCGLEBPVSRYGVYSLTTNCTGRLCNRAPSSQTVGATTSIALGLMLLP 120
QY 121 PRLL 124
DB 121 PRLL 124
XX
RESULT 9
ABJ72241
ID ABJ72241 standard; protein; 124 AA.
XX
AC ABJ72241;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human PRO9862 protein.
XX
KW PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;
KM differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003050448-A1.
XX
PD 13-MAR-2003.
XX
PF 28-AUG-2002; 2002US-00230414.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2003-521818/49.
XX
XX N-PSDB; ABT44239.
XX
PT New nucleic acid encoding for a PRO protein, useful for the manufacture
PT of a medicament for diagnosing or treating tumors or for measuring or
PT detecting expression of an associated gene.
XX

XX
XX Claim 11; Fig 28; 315pp; English.
XX
CC The invention relates to a novel isolated nucleic acid encoding a fully
CC defined PRO polypeptide. The molecules of the invention may be useful for
CC stimulating proliferation or gene expression in pericyte cells or the
CC release of TNF-alpha from human blood. Other possible uses include the
CC stimulation or inhibition of chondrocyte proliferation or
CC differentiation, the stimulation of human dermal fibroblast cell
CC proliferation and the detection of the presence of a tumour within a
CC mammal. Furthermore, the nucleic acid may be useful for the manufacture
CC of a medicament for diagnosing or treating a tumour within a mammal or
CC for measuring or detecting the expression of an associated gene, as well
CC as during gene therapy. The current sequence is that of the human PRO
XX
SQ Sequence 124 AA;
XX
Query Match 100.0%; Score 684; DB 6; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MVLQWLLILVMAIPGTTGVKDCVFCBLTDSMOCPEYMHCGDDEDCFTGHGVAPEGTPV 60
DB 1 MVLQWLLILVMAIPGTTGVKDCVFCBLTDSMOCPEYMHCGDDEDCFTGHGVAPEGTPV 60
QY 61 INKGCLRATSCGLEBPVSRYGVYSLTTNCTGRLCNRAPSSQTVGATTSIALGLMLLP 120
DB 61 INKGCLRATSCGLEBPVSRYGVYSLTTNCTGRLCNRAPSSQTVGATTSIALGLMLLP 120
QY 121 PRLL 124
DB 121 PRLL 124
XX
RESULT 10
ABJ72369
ID ABJ72369 standard; protein; 124 AA.
XX
AC ABJ72369;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human PRO9862 protein.
XX
KW PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte;
KM tumour necrosis factor; proliferation; differentiation; gene therapy;
XX
XX dermal fibroblast.
XX
OS Homo sapiens.
XX
PN US2003027988-A1.
XX
PD 06-FEB-2003.
XX
PF 26-AUG-2002; 2002US-00227884.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2003-503301/47.
XX
XX N-PSDB; ABT44522.
XX
PT New PRO protein encoding nucleic acid, useful for preparing PRO
PT polypeptides and anti-PRO antibodies for detecting the presence of a
PT tumor in a mammal.
XX

Db 121 PRLL 124

RESULT 14
ADB80624 standard; protein; 124 AA.

XX ADB80624;
XX
DT 04-DEC-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO9862.

XX Human; secreted and transmembrane protein; PRO; cytosolic; vulnery;
XX antiarthritic; pericyte cell proliferation;
XX pericyte cell differentiation; chondrocyte cell proliferation;
XX chondrocyte cell differentiation; tumour necrosis factor alpha release;
XX (TNF)-alpha release; dermal fibroblast cell proliferation;
XX dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
XX colon tumour; breast tumour; prostate tumour; rectal tumour;
XX liver tumour; tissue typing; chromosome mapping; gene mapping;
XX gene therapy.

XX Homo sapiens.
XX
PN US2003088068-A1.

XX 08-MAY-2003.
XX
PF 13-AUG-2002; 2002US-00219481.

XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-657982/62.
XX N-PSDB; ADB80623.

XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful in gene therapy, chromosome identification, tissue typing, or as
XX hybridization probes in chromosome and gene mapping.

XX Claim 11, Fig 28; 305pp; English.

XX The invention describes an isolated PRO (secreted and transmembrane)
XX polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are
XX useful for stimulating the proliferation of or gene expression in
XX pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful
XX for stimulating the proliferation or differentiation of chondrocyte
XX cells. PRO231, PRO357, PRO125, PRO155, PRO1306 or PRO1419 polypeptide
XX are useful for stimulating the release of tumour necrosis factor (TNF)-
XX alpha from human blood. PRO982, PRO357, PRO723, PRO1306, PRO1419, PRO214,
XX PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080,
XX PRO1478, PRO1134, PRO826, PRO1005, PRO809, PRO1071, PRO1411, PRO1309,
XX PRO1028, PRO1181, PRO1126, PRO1186, PRO1192, PRO1244, PRO1412,
XX PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1279, PRO1340, PRO1338,
XX PRO1343, PRO1376, PRO1387, PRO1409, PRO1474, PRO1917, PRO1560, PRO1567,
XX PRO1887, PRO1928, PRO3441, PRO1801, PRO4333, PRO3543, PRO3444, PRO4322,
XX PRO9940, PRO6079, PRO9836 or PRO10096 polypeptide are useful for
XX stimulating the proliferation of normal human dermal fibroblasts cells.
XX PRO181, PRO229, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408,
XX PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for
XX inhibiting the proliferation of normal human dermal fibroblast cells. PRO
XX polypeptides such as PRO6004, PRO4981, PRO1174, PRO5778, PRO4332, etc.,
XX are useful for detecting the presence of tumour in a mammal which
XX involves comparing the level of expression of the above PRO polypeptides
XX in a test sample of cells taken from the mammal, and a control sample of
XX normal cells of the same cell type, where a higher level of expression of

CC the PRO polypeptides in the test sample as compared to the control sample
CC is indicative of the presence of tumour in the mammal. The tumour is lung
CC tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. (I) is useful as molecular weight markers, for tissue
CC typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is
CC useful for chromosome and gene mapping or gene therapy. (II) is useful
CC for generating transgenic animals or knock-out animals which are useful
CC screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide
CC is useful for treating bone and/or cartilage disorders (e.g., arthritis,
CC sport injuries). This is the amino acid sequence of a human secreted and
CC transmembrane PRO polypeptide.

XX
XX Sequence 124 AA;
XX
XX

Query Match 100.0%; Score 684; DB 7; Length 124;
Best Local Similarity 100.0%; Pred. No. 2.3e-54;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MVLQWLLLVMALEPGTTGVKDCVFCFLTDSMQCPGTVMHCGDDEDCFTGHGVAPTGPV 60
1 MVLQWLLLVMALEPGTTGVKDCVFCFLTDSMQCPGTVMHCGDDEDCFTGHGVAPTGPV 60
Db

QY 61 INKGCIRATSCGLEBVSRYRGVTSITTNCCRTLCNRAPSSQTVGATTSIALGLMLP 120
61 INKGCIRATSCGLEBVSRYRGVTSITTNCCRTLCNRAPSSQTVGATTSIALGLMLP 120
Db

QY 121 PRLL 124
121 PRLL 124
Db 121 PRLL 124

RESULT 15
ADB73165
ID ADB73165 standard; protein; 124 AA.

XX ADB73165;
XX
AC
XX 04-DEC-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO9862.

XX Human; secreted and transmembrane protein; PRO; cytosolic; vulnery;
XX antiarthritic; pericyte cell proliferation;
XX pericyte cell differentiation; chondrocyte cell proliferation;
XX chondrocyte cell differentiation; tumour necrosis factor alpha release;
XX (TNF)-alpha release; dermal fibroblast cell proliferation;
XX dermal fibroblast cell differentiation inhibitor; tumour; lung tumour;
XX colon tumour; breast tumour; prostate tumour; rectal tumour;
XX liver tumour; tissue typing; chromosome mapping; gene mapping;
XX gene therapy.

XX Homo sapiens.
XX
OS
XX
PN US2003096968-A1.

XX 22-MAY-2003.
XX
PF 29-AUG-2002; 2002US-00232223.

XX 01-JUN-2001; 2001WO-US017800.
XX 29-JUN-2001; 2001WO-US021066.
XX 09-APR-2002; 2002US-00119480.

XX (GETH) GENENTECH INC.

XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2003-765525/72.
XX N-PSDB; ADB73164.

XX New isolated PRO polypeptides useful as molecular weight markers in
XX protein electrophoresis, useful for tissue typing, and for treating

PT arthritis and tumors.

PS Claim 11; Fig 28; 308pp; English.

The invention describes an isolated PRO (secreted and transmembrane) polypeptide (I). PRO982, PRO1160, PRO1187 or PRO1329 polypeptide are useful for stimulating the proliferation of or gene expression in pericyte cells. PRO357, PRO229, PRO1272 or PRO4405 polypeptide are useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO231, PRO357, PRO725, PRO1155, PRO1306 or PRO1419 polypeptide are useful for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood. PRO982, PRO357, PRO725, PRO1306, PRO1419, PRO214, PRO247, PRO337, PRO526, PRO363, PRO531, PRO1083, PRO840, PRO1080, PRO1478, PRO1134, PRO826, PRO305, PRO809, PRO1071, PRO1411, PRO1309, PRO1025, PRO1181, PRO1126, PRO1186, PRO1192, PRO1242, PRO1274, PRO1412, PRO1286, PRO1330, PRO1347, PRO1305, PRO1273, PRO1349, PRO1340, PRO1338, PRO1343, PRO1376, PRO1387, PRO1405, PRO1474, PRO1317, PRO1760, PRO1567, PRO19847, PRO1928, PRO4341, PRO1801, PRO4333, PRO3343, PRO3444, PRO4332, PRO9640, PRO6079, PRO9836 or PRO10096 polypeptide are useful for stimulating the proliferation of normal human dermal fibroblasts cells. PRO181, PRO329, PRO788, PRO1194, PRO1272, PRO1488, PRO4302, PRO4408, PRO5723, PRO5725, PRO7154, or PRO7425 polypeptide are useful for inhibiting the proliferation of normal human dermal fibroblast cells. PRO polypeptides such as PRO6004, PRO94981, PRO7174, PRO5778, PRO4332, etc., are useful for detecting the presence of tumour in a mammal which involves comparing the level of expression of the above PRO polypeptides in a test sample of cells taken from the mammal, and a control sample of normal cells of the same cell type, where a higher level of expression of the PRO polypeptides in the test sample as compared to the control sample is indicative of the presence of tumour in the mammal. The tumour is lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour or liver tumour. (I) is useful as molecular weight markers, for tissue typing, or as therapeutic agents. A polynucleotide (II) encoding (I) is useful for chromosome and gene mapping or gene therapy. (II) is useful for generating transgenic animals or knock-out animals which are useful screening useful reagents. PRO357, PRO229, PRO1272 or PRO4405 polypeptide is useful for treating bone and/or cartilage disorders (e.g., arthritis, sport injuries). This is the amino acid sequence of a human secreted and transmembrane PRO polypeptide.

SQ Sequence 124 AA;

Query Match	100.0%;	Score 684;	DB 7;	Length 124;
Best Local Similarity	100.0%;	Pred. No. 2.3e-54;		
Matches 124;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MYLCWILLLLVMAIP	PETTVGVKDCVCE	LIDSNQCCG	TYMHGDDEDC	CTG	HGVAPG	GPV	60
Db	1	MYLCWILLLLVMAIP	PETTVGVKDCVCE	LIDSNQCCG	TYMHGDDEDC	CTG	HGVAPG	GPV	60
QY	61	INNGCRLRATSCGLE	EPVSYRGV	YSLITNNCC	GRGLCNRP	ASSQTY	MGATSLAL	GLMLP	120
Db	61	INNGCRLRATSCGLE	EPVSYRGV	YSLITNNCC	GRGLCNRP	ASSQTY	MGATSLAL	GLMLP	120
QY	121	PRLL	124						
Db	121	PRLL	124						

Search completed: April 15, 2005, 14:08:12
Job time : 81 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2005, 14:00:50 ; Search time 184 Seconds

(without alignments)
345.097 Million cell updates/sec

Title: US-10-809-654-16

Perfect score: 684

Sequence: 1 MVLGMLLLVLMALPPTTGV.....VGATSLALGLGMLPRILL 124

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	684	100.0	124	2	Q8TDM5
2	463	67.3	127	2	Q80ZG0
3	460	67.3	127	2	Q9DAK7
4	112.5	16.4	125	2	Q9UMP8
5	108	15.8	256	2	Q9D727
6	107.5	15.7	133	2	Q6MG57
7	105	15.4	171	1	E323_MOUSE
8	104.5	15.3	240	1	IBP6_HUMAN
9	104.5	15.3	240	1	IBP6_HUMAN
10	104	15.2	134	2	Q9D7B5
11	102.5	15.0	128	1	LY6D_HUMAN
12	102.5	15.0	382	2	Q9NZJ1
13	101	14.8	127	1	LY6D_MOUSE
14	99	14.5	171	1	E323_HUMAN
15	98.5	14.4	123	1	CD59_PIG
16	97	14.2	123	1	PSCA_HUMAN
17	96.5	14.1	118	1	LYNX_MACMU
18	95	13.9	189	2	Q9PM14
19	93	13.6	119	2	Q6W92
20	92.5	13.5	129	2	Q9NCR0
21	92.5	13.5	153	1	NEUV_FUGRU
22	92.5	13.5	249	2	Q6PEX9
23	92	13.5	127	2	Q9DD23
24	92	13.5	135	2	Q9ZIQ3
25	91.5	13.4	133	2	Q9S688
26	91.5	13.4	134	2	Q6MG58
27	90.5	13.2	125	2	Q6UKB3
28	90.5	13.2	208	2	Q96DR2
29	90.5	13.2	251	2	Q6UWNS
30	89.5	13.1	122	2	Q9NCR4
31	88.5	12.9	123	1	PSCA_MOUSE

32	87.5	12.8	118	2	Q9NCQ7	Q9ncq7 dendroides
33	87	12.7	166	2	Q8KIT6	Q8kit6 mus musculus
34	86.5	12.6	126	1	LY6E_CHICK	Q90986 gallus galli
35	86	12.6	294	2	Q9GYJ3	Q9gyj3 caenorhabditis
36	86	12.6	346	2	Q9S274	Q9s274 mus musculus
37	86	12.6	346	2	Q9U074	Q9u074 homo sapien
38	85.5	12.5	560	2	Q9U013	Q9u013 giardia lam
39	85.5	12.5	966	2	Q22378	Q22378 caenorhabditis
40	84.5	12.4	123	2	Q9NCQ0	Q9ncq0 mus musculus
41	84.5	12.4	123	2	Q9D7U0	Q9d7u0 mus musculus
42	84.5	12.4	136	2	Q9NCR2	Q9ncr2 dendroides
43	84.5	12.4	474	2	Q6B8F1	Q6b8f1 mus musculus
44	84	12.3	119	2	Q64HX7	Q64hx7 oncorhynchus
45	84	12.3	201	2	Q9PRC7	Q9prc7 oxytrichus m

ALIGNMENTS

RESULT 1	PRELIMINARY	PRT	124 AA.
Q8TDM5			
Q8TDM5			
AC	Q8TDM5		
DT	01-JUN-2002 (TrEMBLrel. 21, Created)		
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)		
DT	28-OCT-2004 (TrEMBLrel. 28, Last annotation update)		
DE	Speech acrosomal membrane protein 14 (SPACA4)		
GN	Name=SPACA4; Synonyms=SPACA4; ORFNames=UNQ3046;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_Taxid=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Testis;		
RX	MEDLINE=22791710; PubMed=12788941; DOI=10.1074/jbc.M301713200;		
RA	Shetty J., Wolkowicz M.J., Digilio L.C., Klotz K.L., Hayes F.L.,		
RA	Diekmann A.B., Westbrook V.A., Farris E.M., Hao Z., Coonrod S.A.,		
RA	Flickinger C.J., Herr J.C.;		
RT	"SAMP14, a novel, acrosomal membrane-associated,		
RT	glycosylphosphatidylinositol-anchored member of the Ly-6/urokinase-		
RT	type plasminogen activator receptor superfamily with a role in sperm-		
RT	egg interaction."		
RL	J. Biol. Chem. 278:30506-30515(2003).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Burow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusik A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Umed T.B., Tohyuki S., Carninci P., Prange C.,		
RA	Raba S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mulvaney S.J.,		
RA	Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzyviak M.I., Skalska U., Smalins D.E., Schmeich A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RA	Strausberg R.;		
RL	Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.		

[4]
RN SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Bush J.,
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J.,
Seshagiri S., Stammers L., Singh J., Smith V., Stinson J., Vagtes A.,
Vandlen R., Watnabe C., Wleand D., Woods K., Xie M.H., Yansura D.,
Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
Godowski P.;
RA "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
RL EMBL: AF537321; AAL83950.1; -;
DR EMBL: BC047334; AAL47334.1; -;
DR EMBL: AY358387; AA08753.1; -;
DR Genew; HGNC:16441; SPACA4.
SQ SEQUENCE 124 AA; 13004 MW; 53407C5CCD8FC8BF CRC64;
Query Match 100.0%; Score 684; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 7e-56; Mismatches 0; Indels 0; Gaps 0;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MVLQMLLLVVALPGTGTGVKDCVFCFLTDSMOCPGTYMHCGDDEDCFTGHGVAFGTGPV 60
DB 1 MVLQMLLLVVALPGTGTGVKDCVFCFLTDSMOCPGTYMHCGDDEDCFTGHGVAFGTGPV 60
QY 61 INKGCLRATSCGLEBPVSYGVTYSLTTNCCGTGRLCNRAPSSQTVGATTSIALGLGMLLP 120
DB 61 INKGCLRATSCGLEBPVSYGVTYSLTTNCCGTGRLCNRAPSSQTVGATTSIALGLGMLLP 120
QY 121 PRLL 124
DB 121 PRLL 124
QY 121 PRLL 124
DB 121 PRLL 124
RESULT 2
080200 PRELIMINARY; PRT; 127 AA.
AC Q80200;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE RIKEN cDNA 1700008E09.
GN Name=1700008E09Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22368257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner F.S., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko U., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
Browstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
Rizhak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gumarane P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyniowski M.I., Skalka U., Smalusz D.E., Schnerch A., Schein J.E.,
Jones S.J., Maier M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC048608; AA48608.1; -;
DR MGD; MGI:1916613; 1700008E09Rik.
SQ SEQUENCE 127 AA; 13380 MW; A4871B4A7F8C41B6 CRC64;
Query Match 67.7%; Score 463; DB 2; Length 127;
Best Local Similarity 67.7%; Pred. No. 2.4e-35; Mismatches 25; Indels 2; Gaps 1;
Matches 84; Conservative 13; Mismatches 25; Indels 2; Gaps 1;
QY 1 MVLQMLLLVVALPGTGTGVKDCVFCFLTDSMOCPGTYMHCGDDEDCFTGHGVAFGTGPV 60
DB 1 MVLQMLLLVVALPGTGTGVKDCVFCFLTDSMOCPGTYMHCGDDEDCFTGHGVAFGTGPV 60
QY 61 INKGCLRATSCGLEBPVSYGVTYSLTTNCCGTGRLCNRAPSSQTVGATTSIALGLGMLLP 120
DB 61 INKGCLRATSCGLEBPVSYGVTYSLTTNCCGTGRLCNRAPSSQTVGATTSIALGLGMLLP 120
QY 121 PRLL 124
DB 121 PRLL 124
QY 121 PRLL 122
DB 121 PRLL 122
RESULT 3
09DAK7 PRELIMINARY; PRT; 127 AA.
AC Q9DAK7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:1700008E09 product:hypothetical protein, full insert
DE sequence.
GN Name=1700008E09Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085650; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to

RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Kono H., Akiyama J., Nishi K., Kitanai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Kashiwagi K.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
Yonekura Y., Ishikawa T., Ozawa K., Tanaka T., Matsushita S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayaishizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hamasaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
Imotaka K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayaishizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK005760; BAB24224.1; -
KW MGD; MGI:191613; 170000809Rik.
SQ Hypothetical protein.
SQ SEQUENCE 127 AA; 13408 MW; B3A02B5D58BC41B6 CRC64;
Query Match 67.3%; Score 460; DB 2; Length 127;
Best Local Similarity 66.9%; Pred. No. 4,5e-35;
Matches 83; Conservative 14; Mismatches 25; Indels 2; Gaps 1;
QY 1 MVLWLLLVMLPPTGTVKDCVFCFLTDSMOCPTGYHMGDEDCFTGHGVAFGTGPV 60
DB 1 MVLGMPLLLVLCVPGVTGIXKDCVFCFLTDSARCPGTHMCGDEDCFTGHGVAQGVGPI 60
QY 61 INKGLRATSCGLEEPVSYRGVYSLTTCCTGRLCNRAPSSQTVGATTSIALGLMLP 120
DB 61 INKGVHSTSCGLEEPISYGLTSLTTCCTGRLCNKGTGLST-GATSLSLGLQLLIG 118
QY 121 PRL 124
DB 119 LLLL 122
Db 119 LLLL 122
RESULT 4
Q9UMP8 PRELIMINARY; PRT; 125 AA.
AC Q9UMP8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE G6e protein.
GN Name=G6e;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99316314; PubMed=10384126;
RA Ribas G., Nevill M., Wixon J.L., Cheng J., Campbell R.D.,
RT "Genes encoding three new members of the leukocyte antigen 6
RT superfamily and a novel member of Ig superfamily, together with genes
RT encoding the regulatory nuclear chloride ion channel protein (hRNCC)

RT and an N omega-N omega-dimethylarginine dimethylaminohydrolase
RT homologue, are found in a 30-kb segment of the MHC class III region."
RL J. Immunol. 163:278-287(1999).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22074936; PubMed=12079290; DOI=10.1006/geno.2002.6794;
RA Mallia M., Campbell R.D., Aguado B.,
RT "Transcriptional analysis of a novel cluster of Ly-6 family members in
RT the human and mouse major histocompatibility complex: five genes with
RT many splice forms."
RL Genome Res. 10:113-123(2002).
DR EMBL: AL245419; CAB52193.1; -
SQ SEQUENCE 125 AA; 13524 MW; C09252F9BA822926 CRC64;
Query Match 16.4%; Score 112.5; DB 2; Length 125;
Best Local Similarity 31.9%; Pred. No. 0.0083;
Matches 38; Conservative 11; Mismatches 55; Indels 15; Gaps 5;
QY 1 MVLWLLLVMLPPTGTVKDCVFCFLTDSMOCPTGYHMGDEDCFTGHGVAFGTGPV 60
DB 11 LFLGALGLTMS--PARGRRLCYICGFT--KCHPVPTECRDDEAC---GISIGTS-- 59
QY 61 INKGLRATSCGLEEPVSYRGVYSLTTCCTGRLCNRAPSSQTVGATTSIALGLML 119
DB 60 -GRKSLRAQCPLPGYATYWLHSHYTLMHRCCEQDLNIAASPOL---TSLASLPFLV 114
RESULT 5
Q9D7Z7 PRELIMINARY; PRT; 256 AA.
AC Q9D7Z7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male stomach cDNA, RIKEN full-length enriched
DE library, clone:2210003103 product:weakly similar to METASTASIS-
DE ASSOCIATED GPI-ANCHORED PROTEIN.
GN Name=2210003103Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayaishizaki Y.,
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RA The FANTOM Consortium;
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
[4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Stomach;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Kono H., Okazaki Y., Muramatsu M., Hayaishizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).

RA MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Sherman C.M., Schuller G.D.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuller G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Diatchenko L., Marisla K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uebli T.B., Toshitsuki S., Carninci P., Prange C.,
 RA Raha S.S., Logganiello N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallilou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.J., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzyzanski M.T., Skalska U., Smallus D.E.,
 RA Scherich A., Schein J.E., Jones S.J.M., Maira M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC - SUBCELLULAR LOCATION: Secreted (By similarity).
 CC - SIMILARITY: Contains 1 UPAR/Ly6 domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@1sb-sib.ch).
 CC -----
 DR EMBL: AK053620; BAC35449.1; -
 DR EMBL: BC070462; AA070462.1; -
 DR MGD: MGI:2443848; E130115503Rik.
 DR InterPro: IPR001526; Ly6_UPAR.
 DR SMART: SM00134; LU; 1.
 KM SIGNAL.
 FT SIGNAL. 1 22 By similarity.
 FT CHAIN 23 171 Protein EBP3023.
 FT DOMAIN 47 141 UPAR/Ly6.
 FT CARBOHYD 134 134 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 147 147 N-linked (GlcNAc...) (potential).
 SO SEQUENCE 171 AA; 19065 MW; 2AF86868BDE5CC4 CRC64;
 Query Match 15.4%; Score 105; DB 1; Length 171;
 Best Local Similarity 29.4%; Pred. No. 0.055;
 Matches 42; Conservative 15; Mismatches 46; Indels 40; Gaps 12;
 QY 3 LCVLLLL-----VMALPFGTT---GYKDCVFCF-LTDSMOC-----P 35
 DB 7 LALLLLSLVADCLKAQSRDFVYKDIYHPSITTPYGGFKCTCKADNTECNRMAP 66
 QY 36 GTYMHC-GDDEDCFTGHV-APGTGVPYNGCLATSC--GLEEPVSYRGVYSLTNC 90
 DB 67 DIY--CPDRRYCYCTGHTMEVTSNSISVTRKCVPLEBCLSTGCRDS-EHSG-YKICTSC 121
 QY 91 CTGRLCN-RAPSSQT--VGATTS 110
 DB 122 CEGNICMLPLPRMETATFATTS 144
 RESULT 8
 ID 09H2B5 PRELIMINARY; PRT; 111 AA.
 AC 09H2B5;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Insulin-like growth factor binding protein 6 (fragment).
 GN Name=IGFBP6;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RE SEQUENCE FROM N.A.
 RX MEDLINE=21167382; PubMed=11267670; DOI=10.1016/S0167-4781(01)00192-0;
 RA Daillly Y.P., Zhou Y., Linhart T.A., Baylink D.J., Strong D.D.,
 RT "Structure and characterization of the human insulin-like growth
 RT factor binding protein (IGFBP)-6 promoter: identification of a
 RT functional retinoid response element.";
 RL Biochim. Biophys. Acta 1518:145-151(2001).
 DR EMBL: AF297519; AAC37059.1; -
 DR HSSP: P24593; 1H59.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005520; P:insulin-like growth factor binding; IEA.
 DR GO: GO:0001558; P:regulation of cell growth; IEA.
 DR InterPro: IPR009030; Grow_fac_recept.
 DR InterPro: IPR000867; Ins1_gro_fac_pr.
 DR Pfam: PF00219; IGFBP; 1.
 DR SMART: SM00121; IB; 1.
 DR NON TER 111 111.
 SO SEQUENCE 111 AA; 11236 MW; 235F748AC3C7B946 CRC64;
 Query Match 15.3%; Score 104.5; DB 2; Length 111;
 Best Local Similarity 30.3%; Pred. No. 0.041;
 Matches 37; Conservative 10; Mismatches 50; Indels 25; Gaps 6;
 QY 3 LCVLLLLVMALPFGTTGVNDCVFCFELTDSMOCGTYMHCSDRDCFTGHVAPGTGPVIN 62
 DB 10 LLLLLALLLASFG-GALARCPCGGCGVQACGG---GCVBBD-----GSPREGCAEA 60
 QY 63 KGCICR-ATSCGLEEPVSYRGVYSLTNCCTGRLCNRAPSSQVATTSIALGLMLTP 120
 DB 61 EGCLEAREGECGCVYTP-----NCAPLQGH--PPKDDAPLRLALLGRGRCLP 106
 QY 121 PR 122
 DB 107 AR 108
 RESULT 9
 ID IBP6_HUMAN STANDARD; PRT; 240 AA.
 AC P24592; Q14492;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Insulin-like growth factor binding protein 6 precursor (IGFBP-6) (IBP-
 DE 6) (IGF-binding protein 6).
 GN Name=IGFBP6; Synonyms=IBP6;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Osteosarcoma;
 RX MEDLINE=91225006; PubMed=1709161;
 RA Kleiter M.C., Maslarz F.R., Bauer D.M., Zapf J.,
 RT "Identification and molecular cloning of two new 30-kDa insulin-like
 RT growth factor binding proteins isolated from adult human serum.";
 RL J. Biol. Chem. 266:9043-9049(1991).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=99189142; PubMed=10087296;
 RA Ehrenborg E., Zazzi H., Lagercrantz S., Grandvict M., Hillerbrand U.,
 RA Allander S.V., Larsson C., Luthman H.,
 RT "Characterization and chromosomal localization of the human insulin-
 RT like growth factor-binding protein 6 gene.";
 RL Mamm. Genome 10:376-380(1999).
 RN [3]
 RN SEQUENCE FROM N.A., AND VARIANTS GUY-128 AND GLN-217.
 RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
 RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Foel C.L., Robertson P.D.,

RA Schnackenberg W.S., Sherwood J.K., Mitrak I.A., Nickerson D.A.;
RT "NIHNS-SNPs: environmental genome project, NIHNS ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: <http://esg.gs.washington.edu>).";
RL Submitted (OCT-2003) to the EMBL/Genbank/DBS databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Boone C.K.H., Scheeler C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.S., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Kana S.S., Loquellano N.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Bosnak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heltón E., Kettelman M., Madan A., Rodríguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
RA Buterfield J.Y.S.N., Krzywinski M.J., Skalska U., Smallus D.E.,
RA Schencher A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP SEQUENCE OF 2-240 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=92049376; PubMed=179383;
RA Shimazaki S., Gao L., Shimomaka M., Ling N.;
RT "Isolation and molecular cloning of insulin-like growth factor-binding
RT protein-6.";
RL Mol. Endocrinol. 5:938-948(1991).
RN [6]
RP PARTIAL SEQUENCE OF 28-42.
RC MEDLINE=91207355; PubMed=1850257;
RA Andrews D.L., Birbaumer R.S.;
RT "A novel human insulin-like growth factor binding protein secreted by
RT osteoblast-like cells.";
RL Biochem. Biophys. Res. Commun. 176:213-218 (1991).
RN [7]
RP PRELIMINARY SEQUENCE OF 28-42.
RC TISSUE=Cerebrospinal fluid;
RX MEDLINE=90005986; PubMed=2551722; DOI=10.1016/0014-5793(89)81101-9;
RA Roghiani M., Hossenlupp P., Lepage P., Ballard A., Binoux M.;
RT "Isolation from human cerebrospinal fluid of a new insulin-like growth
RT factor-binding protein with a selective affinity for IGF-II.";
RL FEBS Lett. 255:253-258 (1989).
RN [8]
RP CARBOHYDRATE-LINKAGE SITES.
RC MEDLINE=98241382; PubMed=9572875; DOI=10.1021/bi972894e;
RA Neumann G.M., Marinaro J.A., Bach L.A.;
RT "Identification of O-glycosylation sites and partial characterization
RT of carbohydrate structure and disulfide linkages of human insulin-like
RT growth factor binding protein 6.";
RL Biochemistry 37:6572-6585 (1998).
RN [9]
RP DISULFIDE BONDS.
RX MEDLINE=99262603; PubMed=10329650; DOI=10.1074/jbc.274.21.14587;
RA Neumann G.M., Bach L.A.;
RT "The N-terminal disulfide linkages of human insulin-like growth
RT factor-binding protein-6 (hIGFBP-6) and hIGFBP-1 are different as
RT determined by mass spectrometry.";
RL J. Biol. Chem. 274:14587-14594 (1999).
RN [10]
RP FUNCTION: IGF-binding proteins prolong the half-life of the IGFs
CC and have been shown to either inhibit or stimulate the growth
CC promoting effects of the IGFs on cell culture. They alter the
CC interaction of IGFs with their cell surface receptors.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-linked glycans consist of hexose (probably Gal), N-

```
CC aceeJhexosamine (probably GalNAc) and sialic acid residues. Major
CC glycoforms consist of 8-16 monosaccharides (by homology to IGFBP-6
CC expressed recombinantly in CHO cells).
CC -I SIMILARITY: Contains 1 IGFBP domain.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M62402; AAB06187.1; -.
DR EMBL; AJ006952; CAA07346.1; -.
DR EMBL; AY443494; AAR05445.1; -.
DR EMBL; BC003507; AAH03507.1; -.
DR EMBL; BC005007; AAH05007.1; -.
DR EMBL; BC010162; AAH10162.1; -.
DR EMBL; BC011708; AAH11708.1; -.
DR EMBL; M69054; AAA88070.1; -.
DR PIR; A39842; A39842.
DR PIR; S05699; S05699.
DR HSSP; P24593; LBOE.
DR GeneW; HGNC:5475; IGFBP6.
DR MIM; 146735; -.
DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
DR InterPro; IPRO09030; Grow_fac_recept.
DR InterPro; IPRO09168; IGFBP1-6.
DR InterPro; IPRO00867; Insl_gro_fac_pr.
DR InterPro; IPRO00716; Thyroglobulin_1.
DR Pfam; PF00219; IGFBP, 1.
DR Pfam; PF00086; Thyroglobulin_1; 1.
DR PIRSF; PIRSF001969; IGFBP1-6; 1.
DR SMART; SM00121; IB; 1.
DR SMART; SM00211; TY; 1.
DR PROSITE; PS00222; TGF_BINDING; FALSE NEG.
DR PROSITE; PS00484; THYROGLOBULIN_1; 1.
KW Polypeptide chain sequencing; Glycoprotein; Growth factor binding;
KW Polyomorphism; Signal.
FT SIGNAL 1 24
FT CHAIN 25 240
FT FT Insulin-like growth factor binding protein 6
FT FT Thyroglobulin type-I.
FT DOMAIN 186 234
FT FT DISULFID 29 32
FT FT DISULFID 40 44
FT FT DISULFID 57 63
FT FT DISULFID 71 84
FT FT DISULFID 78 104
FT FT DISULFID 163 190
FT FT DISULFID 201 214
FT FT DISULFID 214 234
FT CARBOHYD 126 126
FT CARBOHYD 144 144
FT CARBOHYD 145 145
FT CARBOHYD 146 146
FT CARBOHYD 152 152
FT VARIANT 128 128 /FTid=VAR_018932.
FT VARIANT 217 217 R->Q.
FT VARIANT 236 236 /FTid=VAR_018933.
FT VARIANT 236 236 T->P (in dSNP:1053134).
FT CONFLICT 2 2 /FTid=VAR_011907.
SQ SEQUENCE 240 AA; 25322 MW; 285308231C025009 CRC64;
Query Match 15.3%; Score 104.5; DB 1; Length 240;
Best Local Similarity 30.3%; Pred. No. 0.084;
Matches 37; Conservative 10; Mismatches 50; Indels 25; Gaps 6;
3 LCWILLVLMALPRGTGVKDCVFCECLDSMQCGTYMHGCDDBDCEFGHGVAQTGPVIN 62
| | | : : : | | : | | | | | : : : | | | | |
```


Db 10 LLLLLLLLLASPG-GALANCPGCGGVQAGCPG---GCVEEBD-----GGSPAEGCAEA 60
 Qy KGCGR-ATSCGLEPVSRYGVYSLTTNCTGRLCNRAPSSQTVGATSLALGMLLP 120
 Db 61 EGCRLREGCGECGVYTP-----NCAPIGQCH-PPKDEADPLRALLLGRGCLP 106
 Qy 121 PR 122
 Db 107 AR 108
 RESULT 10
 Q9D7E5 PRELIMINARY; PRT; 134 AA.
 ID Q9D7E5
 AC Q9D7E5
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Mus musculus adult male tongue cDNA, RIKEN full-length enriched
 DE library, clone:231001102 product:putative Ly-6 superfamily member,
 DE full insert sequence (ly6g6e protein, isoform A).
 GN Name=ly6g6e;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxId=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RA The FANTOM Consortium;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagasaki S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kikunaka T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto S., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujisake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsumura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 [6]
 RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RA Aachai J., Aizawa K., Carninci P., Akiyama T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirakata T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=22074936; PubMed=12079290; DOI=10.1006/geno.2002.6794;
 RA Mallya M., Campbell R.D., Aguado B.;
 RT "Transcriptional analysis of a novel cluster of Ly-6 family members in
 RT the human and mouse major histocompatibility complex: five genes with
 RT many splice forms";
 RL Genomics 80:113-123(2002).
 DR EMBL; AK009303; BAB26204.1; -;
 DR EMBL; AJ315550; CAC85546.1; -;
 DR MCD; MG1:1917524; Ly6g6e.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005024; F:transforming growth factor beta receptor ac. .; IEA.
 DR InterPro; IPR000472; Activin_receptor.
 DR InterPro; IPR001526; Ly6_UPAR.
 DR Pfam; PF01064; Activin_1recp; 1.
 DR SMART; SM00134; LV; 1.
 SQ SEQUENCE 134 AA; 14600 MW; 4669A7BBB5DBD30 CRC64;
 Query Match 15.2%; Score 104; DB 2; Length 134;
 Best Local Similarity 31.0%; Pred. No. 0.055;
 Matches 31; Conservative 7; Mismatches 42; Indels 20; Gaps 4;
 Qy 16 GTTGVD-----VPCFELTDMQCPGYMHCGDEDCFTSHGVAPGTGP-----VI 61
 Db 15 GTTGLTTPARKRLRYTCSF-AKPCDVPKRCRDENV-----GVSVGTSQKEREVIE 68
 Qy 62 NKGCRLATSCGLEPVSRYGVYSLTTNCTGRLCNRAPSS 101
 Db 69 RKGCRLPACCPILGHATVWSRSYSLRHCCEDLCNAAS 108
 RESULT 11
 LY6D HUMAN STANDARD; PRT; 128 AA.
 ID LY6D HUMAN
 AC Q14210; Q43783; O8TBd4; Q92933;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Lymphocyte antigen Ly-6D precursor (E48 antigen).
 GN Name=LY6D; Synonyms=E48;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 ON NCBI_TaxId=9606;
 [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 21-33.
 RX MEDLINE=9531036; PubMed=7790363; DOI=10.1083/jcb.129.6.1677;
 RA Brakenhoff R.H., Gerretsen M., Knippels E.M.C., van Dijk M.,
 RA van Esen H., Weghuis D.O., Sinke R.J., Snow G.B.,
 RA van Dongen G.A.M.S.;
 RT "The human E48 antigen, highly homologous to the murine Ly-6 antigen
 RT THB, is a GPI-anchored molecule apparently involved in keratinocyte
 RT cell-cell adhesion";
 RL J. Cell Biol. 129:1677-1689(1995).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98031741; PubMed=9366413;
 RA Brakenhoff R.H., van Dijk M., Roode-Knippels E.M.C., Snow G.B.;

RT "A galinof novel tissue specificity in the human Ly-6 gene E48.",
 RL J. Immunol. 159:4879-4886(1997).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zedberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stepien M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Paley J., Heltón E., Kettelman M., Madan A.C., Rodríguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RN SEQUENCE OF 18-96 FROM N.A.
 RP Shan X., Bourdeau A., Rhoton A., Wells D.E., Cohen E.H.,
 RA Landgraf B.E., Palfrey R.G.E.;
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RN SEQUENCE OF 21-35.
 RP PubMed=15340161; DOI=10.1110/ps.04682504;
 RX Zhang Z., Henzel W.J.;
 RA "Signal peptide prediction based on analysis of experimentally
 RT verified cleavage sites".
 RL Protein Sci. 13:2819-2824(2004).
 CC -1- FUNCTION: May be involved in cell-cell adhesion and signal
 CC transduction.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -1- TISSUE SPECIFICITY: Expressed exclusively at the outer cell
 CC surface of transitional epithelia and the keratinocyte of
 CC stratified squamous epithelia.
 CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.
 CC -----
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 CC -----
 CC EMBL, X82693, CAA58014.1, -,
 DR EMBL, Y12642, CAA73189.1, -,
 DR EMBL, BC022806, AAH22806.1, ALY_INIT.
 DR EMBL, U66837, AAB07524.1, -,
 DR PIR, A57321, A57321.
 DR Genew, HGNC:13348, LY6D.
 DR H-InvDB, HIX0007832, -.
 DR MIM, 606204, -,
 DR GO, GO:0005624, C:membrane fraction; TAS.
 DR GO, GO:0007155, P:cell adhesion; TAS.
 DR InterPro, IPR003632, Ly-6 CD59.
 DR InterPro, IPR001526, Ly6 UPAR.
 DR Pfam, PF00021, UPAR_Ly6; 1.
 DR SMART, SMO0134, LU; 1.
 DR PROSITE, PS00983, Ly6 UPAR; 1.
 KM Antigen; Cell adhesion; Direct protein sequencing; GPI-anchor;
 KM Lipoprotein; Membrane; Multigene family; Signal.
 RT SIGNAL
 RT 1 20
 RT CHAIN 21 98 Lymphocyte antigen Ly-6D.

FT	PROPEIN	99	128	Removed in mature form (Potential) .
FT <td>DOMAIN</td> <td>21</td> <td>108</td> <td>UPAR/Ly6.</td>	DOMAIN	21	108	UPAR/Ly6.
FT	DISULFID	23	45	By similarity.
FT	DISULFID	26	32	By similarity.
FT	DISULFID	28	63	By similarity.
FT	DISULFID	67	86	By similarity.
FT	DISULFID	87	92	By similarity.
FT	LIPID	98	98	GPI-anchor amidated asparagine (Potential)
FT	CONFLICT	10	10	A -> T (in Ref. 2).
FT	CONFLICT	60	60	K -> E (in Ref. 4).
FT	CONFLICT	76	76	Q -> L (in Ref. 4).
FT	SEQUENCE	128 AA;	13286 MW;	39618DF6A5B0EBD CRC64;
Query Match		15.0%;	Score 102.5;	DB 1; Length 128;
Best Local Similarity		28.3%;	Pred. No. 0.072;	
Matches	36;	Conservative	19;	Mismatches 59; Indels 13; Gaps 4
Qy	6	LLLLVMAALPPTGTGKDCVFCCLTDSMCCPGTYMHGCDDEDCFTGHGVAFGTGPVINKGC	65	
Db	6	LLLAALAVATPALTLRCHVC--TSSNCKHSVVCPSASSPFKKTINTVEPLRGNLVKKDC	63	
Qy	66	LRATSCGLEEPVSYRGVTVSLTNTCTGRLCN---RAPSSQTGATTSIALGLGN----	117	
Db	64	--ASCTPSYTLQGVSSGSTSTGCCQCDLQNEKLHNAAPRTALAHSAISGLALSILA	121	
Qy	118	-LLPPRL 123		
Db	122	VILAPSL 128		
RESULT 12				
Q9NZJ1	PRELIMINARY;	PRT;	382 AA.	
Q9NZJ1	AC			
DT	01-OCT-2000 (TREMBlrel. 15, Created)			
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)			
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)			
DE	Megakaryocyte-enhanced gene transcript 1 protein.			
GN	Name=MEG11;			
OS	Homo sapiens (Human) .			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
CK	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Mueller R., Ziegler B.L.;			
RL	Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF195764; AAF5181.1; .			
DR	InterPro; IPR003599; IG-like.			
DR	InterPro; IPR007110; IG-like.			
DR	SMART; SM00409; IG_1.			
DR	PROSITE; PS50835; IG LIKE; 1.			
SEQ	SEQUENCE 382 AA; 40892 MW; 6BE11B91E760C8CF CRC64;			
Qy	Query Match	15.0%;	Score 102.5;	DB 2; Length 382;
Best Local Similarity		25.3%;	Pred. No. 0.2;	
Matches	37;	Conservative	13;	Mismatches 63; Indels 33; Gaps 5
Qy	5	WLLLVMAAL-----PPTGTGKDCVFCCLTDSMCCPGTYMHGCD	44	
Db	235	WILLMLLMGGVITALISIVLMRQVARGAERGGRNRCYNGGSPSSCKEAVTTCCGG	294	
Qy	45	EDCFTGHGV---APGTGPVI---NKGCLRATSCGLEEPVSYRGVTVSLTNTCTGRLC	96	
Db	295	R---PQGLBEIKIKPGRNPFTVLIHQHRCQVAANHNGVETSSVGDVTVPAHNDCTVLGDL	351	
Qy	97	NRAPSSQT--VGATTSIALGLGLLP 120		
Db	352	NSAVASHVAPAGILAAATAATLTCLLP 377		
RESULT 13				

us-10-809-654-16.rup

KW PROSITE PS00983; Ly6 UPAR; 1.
 Antigen; GPI-anchor; Lipoprotein; Membrane; Multigene family; Signal.
 FT SIGNAL 1 20 Potential.
 FT CHAIN 21 98 Lymphocyte antigen Ly-6D.
 FT PROPEP 99 127 Removed in mature form (Potential).
 FT DOMAIN 21 108 UPAR/Ly6.
 FT DISULFID 23 45 By similarity.
 FT DISULFID 26 32 By similarity.
 FT DISULFID 38 63 By similarity.
 FT DISULFID 67 86 By similarity.
 FT DISULFID 87 92 By similarity.
 FT LIPID 98 98 GPI-anchor amidated serine (Potential).
 SQ SEQUENCE 127 AA; 13395 MW; 0AF039B7D105917 CRC64;
 Query Match 14.8%; Score 101; DB 1; Length 127;
 Best Local Similarity 31.4%; Pred. No. 0.099;
 Matches 37; Conservative 12; Mismatches 55; Indels 14; Gaps 4;
 Db 66 LRLATSCGLEPVPVSYRGVYSLTTNCCGRLCNR-----AP-----SSQTVGATTSAL 113
 6 LVLLVLAIVAVTSPAMALRCHVC--TNSANCKNPQVCPSPNFFCKTVTYSVEPLNGLVKKEC 63
 64 --ANSCSDVSGQGHVSSGSEVYQCCTDLCNELVSAAGHALLSVTGLATSLSI 119
 RESULT 14
 ID E323 HUMAN STANDARD; PRT; 171 AA.
 AC 066778;
 DT 25-JAN-2005 (Rel. 46, Created)
 DT 25-JAN-2005 (Rel. 46, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Protein BPGP3023 precursor (UNQ3023/PRO9821).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN 1;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22867296; PubMed=12975309; DOI=10.1101/gt.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Batton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seehagiri S., Simone L., Singh V., Smith V., Stinson J., Vagts A.,
 RA Vanden R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,
 RA Yi S., Yu G., Yuan Y., Zhang M., Zhang Z., Goddard A., Wood W.T.,
 RA Godowski P., Gray A.;
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN 1;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hulteh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Sapich M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toehiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Hult S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fehey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.;

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RN SEQUENCE OF 23-37.
RX PubMed=15340161; DOI=10.1110/ps.04682504;
RA Zhang Z., Henzel W.J.;
RT "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites";
RL Protein Sci. 13:2819-2824(2004).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.
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CC -----
DR EMBL, AF358623; AAC08986.1; -;
DR EMBL, BC047013; AAH47013.1; -;
KW Direct protein sequencing; Signal.
FT SIGNAL 1 22
FT CHAIN 23 171 Protein BRP3023.
FT DOMAIN 47 141 UPAR/Ly6.
FT CARBOHYD 134 134 N-linked (GlcNAc..) (Potential).
FT CARBOHYD 147 147 N-linked (GlcNAc..) (Potential).
SQ SEQUENCE 171 AA; 19118 MW; 1BAEBE9CD18F5470 CRC64;
Query Match 14.5%; Score 99; DB 1; Length 171;
Best Local Similarity 25.3%; Pred. No. 0.2; Mismatches 49; Indels 58; Gaps 12;
Matches 43; Conservative 20; Mismatches 49; Indels 58; Gaps 12;
QY 3 LCMALL-----VMALPPTGTT--GVKDCVFCE-LTDSMOC-----P 35
DB 7 LAMLLLSLLADCLKAQNSDFTVVKDIIYLHPSTTPYGGFKFCEKADNVECRMAP 66
QY 36 GYIMAC-GGDEDCFTGHG-V-APGTGVINKGCLRAISC--GLAEFVSTRGVTSLTNC 90
DB 67 DLY--CPRETRYCYTHMEVTNNSIVTKRCVPLEECLSTGGRDS-EHGG--HKVCTSC 121
QY 91 CTGRLCN-----RAPSSQTVG-----ATTSLALGGMLL 119
DB 122 CEGNLCNLPFPRNETATPATTSPINQTHGPRCMGVIVSCLMWLGLML 171
RESULT 15
CD59_PIG STANDARD; PRT; 123 AA.
AC 062680; Q9TR76; Q9XT94;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE CD59 glycoprotein precursor (Membrane attack complex inhibition
DE factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
GN Name=CD59;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sub.
OC NCBI_TaxID=9823;
OC RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aortic endothelium;
RX MEDLINE=98217182; PubMed=9558099;
RA Hinchliffe S.J., Rushmere N.K., Hanna S.M., Morgan B.P.;
RT "Molecular cloning and functional characterization of the pig analogue
RT of CD59, relevance to xenotransplantation.";
RL J. Immunol. 160:3924-3932(1998).

RN [2]
RN SEQUENCE OF 26-123 FROM N.A., AND FUNCTION.
RC TISSUE=Aortic endothelium;
RX MEDLINE=99023683; PubMed=9808497;
RA Maher S.E., Pflugh D.L., Larsen N.J., Rothschild M.F.,
RA Botwell A.L.M.;
RT "Structure/function characterization of porcine CD59: expression,
RT chromosomal mapping, complement-inhibition, and costimulatory
RT activity.";
RL Transplantation 66:1094-1100(1998).
RN [3]
RN SEQUENCE OF 26-64.
RC TISSUE=Erythrocyte;
RX MEDLINE=95181826; PubMed=7533195; DOI=10.1016/0022-1759(94)00288-8;
RA van den Berg C.W., Harrison R.A., Morgan B.P.;
RT "A rapid method for the isolation of analogues of human CD59 by
RT preparative SDS-PAGE: application to pig CD59.";
RL J. Immunol. Methods 179:223-231(1995).
CC -1- FUNCTION: Potent inhibitor of the complement membrane attack
CC complex (MAC) action. Acts by binding to the C8 and/or C9
CC components of the assembling MAC, thereby preventing
CC incorporation of the multiple copies of C9 required for complete
CC formation of the osmolytic pore.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- TISSUE SPECIFICITY: Expressed in all tissues tested (lung, testis
CC liver, kidney, spleen, heart and skeletal muscle). Highest levels
CC in lung and spleen, lowest levels in liver and skeletal muscle.
CC -1- SIMILARITY: Contains 1 UPAR/Ly6 domain.
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DR EMBL, AF020302; AAC67231.1; -;
DR EMBL, AF058328; AAD39837.1; -;
DR HSSP, P13987; 1ERG.
DR InterPro: IPR003632; Ly-6 CD59.
DR InterPro: IPR001526; Ly6 UPAR.
DR Pfam: PFO0021; UPAR_Ly6_1.
DR ProDom: PDD003128; Ly-6_CD59_1.
DR SMART; SM00134; L0; 1.
DR PROSITE; PS00983; Ly6 UPAR; 1.
KW Antigen; Direct protein sequencing; Glycoprotein; GPI-anchor;
KW Lipoprotein; Signal
FT SIGNAL 1 25
FT CHAIN 26 98
FT PROPEP 99 123
FT DOMAIN 26 103
FT DISULFID 28 51
FT DISULFID 31 38
FT DISULFID 44 65
FT DISULFID 71 89
FT DISULFID 90 95
FT CARBOHYD 43 43
FT CARBOHYD 98 98
FT LIPID 26 26
FT CONFLICT 46 46
FT CONFLICT 63 63
SQ SEQUENCE 123 AA; 13790 MW; FDE2ED3F93C91321 CRC64;
Query Match 14.4%; Score 98.5; DB 1; Length 123;
Best Local Similarity 27.0%; Pred. No. 0.16; Mismatches 47; Indels 27; Gaps 6;
Matches 33; Conservative 15; Mismatches 47; Indels 27; Gaps 6;
QY 2 VLCLMLLVMALPPTGVKDCVFCELTDSMOC-----PG-----TYMGGDED-CFTGH 51
DB 8 ILMLLSLT-----AVLCHLGHSLGVCNCINAGSCTTAMNCSHQDADIFVE 55
QY 52 GVAPGTGVINKGCLRAISCGLEEFVSTRGVTSYLTNCCTGRLCNRAPSSQTVGATISL 111

Db 56 APPKT-----YQCMRPEDCNPDF-ISRNLAEKKLKYNCCKDKDCNKS DATISSGTALL 110
Qy 112 AL 113
Db 111 VI 112

Search completed: April 15, 2005, 14:04:11
Job time : 193 secs

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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: April 15, 2005, 14:00:50 ; Search time 16 Seconds
(without alignments)

745.680 Million cell updates/sec

Title: US-10-809-654-16

Perfect score: 684
Sequence: 1 MWLWLLVLMALPGTTGV.....VGATTSIALGLWLLPRL 124

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104.5	15.3	240	2 A39842	insulin-like growth
2	102.5	15.0	128	1 A57321	B48 antigen precursor
3	101	14.8	127	1 A46528	phosphatidylinositol
4	101	14.8	130	2 I54553	gene Thb protein -
5	85.5	12.5	1101	2 T16840	hypothetical prote
6	84	12.3	240	2 T25641	hypothetical prote
7	82.5	12.1	4543	1 A53102	alpha-2-macroglobu
8	80.5	11.8	222	2 B41643	urokinase-type pla
9	80.5	11.8	222	2 B55356	urokinase-type pla
10	80.5	11.8	337	2 A55356	urokinase-type pla
11	80.5	11.8	330	1 JN0561	urokinase-type pla
12	80.5	11.8	1111	2 T26972	hypothetical prote
13	80.5	11.8	1381	2 T20406	hypothetical prote
14	78.5	11.5	1620	2 T27283	hypothetical prote
15	78	11.4	328	2 S42152	urinary plasminoge
16	77.5	11.4	509	2 I59576	transforming growt
17	77.5	11.3	516	2 A48678	activin receptor I
18	77.5	11.3	685	2 JCT570	delta-4 protein -
19	77	11.3	61	1 N1N73E	short neurotoxin 3
20	77	11.3	312	2 T31834	hypothetical prote
21	77	11.3	503	2 A49432	activin receptor-1
22	77	11.3	513	2 S28358	presore vesicle p
23	76	11.1	83	2 S19951	neurotoxin-like pe
24	76	11.1	5376	2 T42215	zonadhesin - mouse
25	75.5	11.0	128	1 RWH59	surface glycoprote
26	75.5	11.0	2160	2 T29764	hypothetical prote
27	75	11.0	61	1 N1N04E	short neurotoxin 4
28	75	11.0	134	2 I48639	neurotoxin homolog
29	75	11.0	509	2 A45992	activin A receptor

30	74	10.8	122	2 PNO622	insulin-like growth
31	74	10.8	136	2 I49013	chymic shared anti
32	74	10.8	248	2 T31841	hypothetical prote
33	74	10.8	509	2 A49664	activin type I rec
34	73.5	10.7	81	2 S27366	metallothionein E
35	73.5	10.7	158	2 B34132	vasotocin / neurop
36	73	10.7	161	2 A46189	vasotocin - Pacifi
37	72.5	10.6	82	2 JCS892	cobrotoxin b - Chi
38	72.5	10.6	134	2 A25708	ly-6.1 protein pre
39	72.5	10.6	603	2 S28941	coagulation factor
40	72.5	10.6	1252	2 S36016	oocyte wall protei
41	72	10.5	249	2 T31837	hypothetical prote
42	72	10.5	496	2 T41114	urotophyrin methy
43	71.5	10.5	153	2 A34132	vasotocin / neurop
44	71.5	10.5	559	1 A29941	c-plasminogen acti
45	71.5	10.5	1321	2 JE0352	mucin MUC5B, trach

ALIGNMENTS

RESULT 1
A39842
insulin-like growth factor-binding protein 6 precursor - human
N/Alternate names: IGFBP-6, insulin-like growth factor II-binding protein
C/Dates: 20-Mar-1992 #sequence revision 31-Dec-1995 #text_change 09-Jul-2004
C/Species: Homo sapiens (man)
A/Accession: A39842; B23734; PH0144; A35470; C35803
R/Kleier, M.C.; Maslitz, F.R.; Bauer, D.M.; Zapf, J.
J. Biol. Chem. 265, 9043-9049, 1991
A/Title: Identification and molecular cloning of two new 30-kDa insulin-like growth factor
A/Reference number: A39842; PMID:91225006; PMID:1709161
A/Accession: A39842
A/Molecule type: mRNA
A/Residues: 1-240 <KIE>
A/Cross-references: UNIPROT:P24592; GB:M62402; NID:G184813; PIDN:AAB06187.1; PID:G184814
R/Shimasaki, S.; Gao, L.; Shimonaka, M.; Ling, N.
Mol. Endocrinol. 5, 938-948, 1991
A/Title: Isolation and molecular cloning of insulin-like growth factor-binding protein-6.
A/Reference number: A23734; PMID:92049376; PMID:1719383
A/Accession: B23734
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 'C', 3-240 <SHI>
A/Cross-references: GB:M69054; NID:G183893; PIDN:AAA8070.1; PID:G183894
R/Andress, D.L.; Birnbaum, R.S.
Biochem. Biophys. Res. Commun. 176, 213-218, 1991
A/Experimental source: cell line V-2
R/Martin, J.L.; Willetts, K.E.; Baxter, R.C.
J. Biol. Chem. 265, 4124-4130, 1990
A/Title: Purification and properties of a novel insulin-like growth factor-II binding pr
A/Reference number: A35470; PMID:90154107; PMID:2154495
A/Accession: A35470
A/Status: preliminary
A/Molecule type: protein
A/Residues: 28, 'A', 30-39 <MAR>
R/Zapf, J.; Kleier, M.; Merryweather, J.; Maslitz, F.; Bauer, D.; Born, W.; Fischer, J.A.
J. Biol. Chem. 265, 14892-14898, 1990
A/Title: Isolation from adult human serum of four insulin-like growth factor (IGF) bindin
A/Reference number: A35803; PMID:90368661; PMID:1697583
A/Accession: C35803
A/Status: preliminary
A/Molecule type: protein
A/Residues: 'AA', 30-31, 'H', 33-54, 'QXC' <ZAP>
C/Genetics: GDB:IGFBP6
A/Genes: GDB:IGFBP6
A/Cross-references: GDB:127456; OMIM:146735

A:Map position:13pter-13qter
C:Superfamily: insulin-like growth factor binding protein; thyroglobulin type I repeat h
E:Keywords: glycoprotein
F:1-37/Domains: signal sequence #status predicted <STR>
F:28-240/Product: insulin-like growth factor-binding protein 6 #status predicted <MAT>
F:163-234/Domains: thyroglobulin type I repeat homology <THYI>
F:123/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	15.3%;	Score 104.5;	DB 2;	Length 240;
Best Local Similarity	30.3%;	Pred. No. 0.032;		
Matches 37;	Conservative 10;	Mismatches 50;	Indels 25;	Gaps 6;

QY	3	LCMTLLVLMALPGHTTGKDCVFCFGLTDSMQCPGTHMCGDDEDCFTGHGVA	PGTHPIN	62
Db	10	LLLLLALTLASPG-GALARCPCGGQVQACPG--GCTVEED-----GGS	PARGCABA	60
QY	63	KGCH--ATSCGLEEPVSYRGVTSLTNNCCGRLCNRAPSSQTVGATTSIALGLMLP		120
Db	61	EGCARRSQEGCGVYTP-----NCAPGLQCH--PRXDEAPILALLHGRCLP		106
QY	121	PR	122	
Db	107	AR	108	

RESULT 2
A57321

E48 antigen precursor - human
N:Alternate names: desmoglein III
C:Species: Homo sapiens (man)
C:Date: 08-Dec-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: A57321
J:Brakehoeft, R.H.; Gerretsen, M.; Knipfels, E.M.C.; van Dijk, M.; van Essen, H.; Olde W.
J. Cell Biol. 129, 1677-1689, 1995
A:Title: The human E48 antigen, highly homologous to the murine Ly-6 antigen Thb, is a G
A:Reference number: A57321, MUID:95310346; PMID:7790363
J:Accession: A57321

A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-128 <BBA>
A:Cross-references: UNIPROT:Q14210, GB:XB2693, NID:g887453, P1DN:CAA58014.1, P1D:g88745454
A:Note: parts of this sequence, including the amino end of the mature protein, were com
C:Genetics:
A:Map position: 8q24-qter
C:Superfamily: Ly-6 antigen; Ly-6 homology
C:Keywords: blocked carboxyl end, cell adhesion; glycoprotein; lipoprotein; phosphatidyl
/1-20/Domain: signal sequence #status #status <Sig>

F:21-100/Domain: Ly-6 homology <Ly6>
F:21-93/Product: E48 antigen #status predicted <MAT>
F:22-45,26-32,38-63,67-86,87-92/Disulfide bonds: #status predicted
F:93/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form)

Query Match	15.0%;	Score 102.5;	DB 1;	Length 128;
Best Local Similarity	28.3%;	Pred. No. 0.029;		
Matches 36;	Conservative 19;	Mismatches 59;	Indels 13;	Gaps 4;

[illegible]

RESULT 3
A46528
phosphatidylinositol-anchored B-cell antigen Thb precursor - mouse
;Alternate names: thymocyte B-cell antigen Thb

C/Species: Mus musculus (house mouse)
C/Date: 18-Jun-1993 #sequence_rev15n 16-Aug-1996 #ext_change 09-Jul-2004
C/Accession: A46528
R/Gmley, T.P.; McKenzie, I.F.; Kozak, C.A.; Sandlin, M.S.
J. Immunol. 149, 2615-2618, 1992
A/Title: Isolation and Characterization of cDNA clones for the mouse thymocyte B cell antigen B220
A/Reference number: A46528; PMID:93017863; PMID:1401899
A/Accession: A46528

A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-127 <GNM>
A:Cross-references: UNIPROT:P35459; GB:M63782; GB:S46666; NID:Z288264; PIDD:CAA5317.1; 7
A:Experimental source: C57BL/6, spleen cells, thymocytes (NCICP.116104)
A:Note: sequence extracted from NCBI backbone (NCICP.116104)
C:Comment: This 15k GPI-anchored surface antigen is found on B thymocytes and B cells.
/Genetics:

A/Gene: Thb
A/Map position: 15
C/Superfamily: Ly-6 antigen; Ly-6 homology
C/Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkage
F1-20/Domain: signal sequence #status predicted <StG>
F12-100/Domain: Ly-6 homology <Ly6>
F12-99/Product: phosphatidylinositol-anchored B-cell antigen Thb #status predicted <MAT>
F19-127/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F99/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form)

Query Match	14.8%;	Score 101;	DB 1;	Length 127;
Best Local Similarity	31.4%;	Pred. No. 0.039;		
Matches 37;	Conservative 12;	Mismatches 55;	Indels 14;	Gaps 4

QY 6 LLLIIVNALPFGTTGVNDVCFCECLTDSMOCPGTYMHCGDDEDCFTGGVAAGTGPVINKG 6
 Db 6 LVYLVIVAAVAPSPAMALRCHVC--TNSANCNPDPVCCSNFXYCFKTVTSVBLEINMLVRKEC 63
 QY 66 LRATSCGLEPRVSYRGVTYSLTNNCTGRLCNN---AP-----SSQTGATTTAL 113
 Db 64 --ANSCSDVDSQGHVSSGSEBVYQCCQTDLCNERIVSAAPGHALLSVYLGATLSL 119

RESULT 4

gene TnB protein - mouse
154553
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 23-Jul-1999
C:Accession: 154553
R:Gumley, T. P.; McKenzie, I. F.; Sandrin, M. S.
J. Biol. Chem. 271: 1096-1100, 1996

Immunogenetics 42, 221-224, 1995
 A;Title: Sequence and structure of the mouse Thb gene.
 A;Reference number: 154553; MUID:95619850; PMID:7642335
 A;Accession: 154553
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-130 <RES>
 A;Cross-references: GB:LI0419; NID:G1019624; PIDR:AAA79249.1; PID:G1019625
 C;Genetics:
 A;Gene: Thb
 A;Intons: 21/1, 54/1
 C;Superfamily: Ly-6 antigen, Ly-6 homology
 C;24-103/Domains: Ly-6 homology <Ly6>

Query Match 14.8%; Score 101; DB 2; Length 130;
 Best Local Similarity 31.4%; Pred. No. 0.039;
 Matches 37; Conservative 12; Mismatches 55; Indels 14; Gaps 4.

QY LLLLLVMAIPGPTGGVKDQVCFCELDSDMQCPGYTMHGGDDEDCFTGHGAPGAPGVINKQC 65
DB LVLLVLLAVLAAVSPMAALRCHVC--TNSANCKMPQVCPSPNFCEPKTVTSLEPENGMLVAREDC 66
QY LRAVTSGLAEBSVPSRGVYTSLLTNCCGGRICNLR-----AP-----SSQTVGATTSIAL 113
67--ANSCSDVDSQOQHVSAGSGSEVTDCCCTDLCENELVLSAAPEHALLSVTLGIANSLSL 122

F:2424-2467/Domain: LDL receptor YWTD-containing repeat homology <YW33>
F:2476-2511/Domain: EGF homology <EG10>
F:2518-2555/Domain: LDL receptor ligand-binding repeat homology <LDLB>
F:2560-2594/Domain: LDL receptor ligand-binding repeat homology <LDLC>
F:2599-2633/Domain: LDL receptor ligand-binding repeat homology <LDLD>
F:2646-2682/Domain: LDL receptor ligand-binding repeat homology <LDLE>
F:2690-2724/Domain: LDL receptor ligand-binding repeat homology <LDLF>
F:2732-2767/Domain: LDL receptor ligand-binding repeat homology <LDLG>
F:2772-2810/Domain: LDL receptor ligand-binding repeat homology <LDLH>
F:2816-2851/Domain: LDL receptor ligand-binding repeat homology <LDLI>
F:2856-2895/Domain: LDL receptor ligand-binding repeat homology <LDLJ>
F:2902-2936/Domain: LDL receptor ligand-binding repeat homology <LDLK>
F:2941-2977/Domain: EGF homology <EG11>
F:2983-3018/Domain: EGF homology <EG12>
F:3066-3110/Domain: LDL receptor YWTD-containing repeat homology <YW35>
F:3111-3153/Domain: LDL receptor YWTD-containing repeat homology <YW36>
F:3154-3197/Domain: LDL receptor YWTD-containing repeat homology <YW37>
F:3198-3238/Domain: LDL receptor YWTD-containing repeat homology <YW38>
F:3239-3281/Domain: LDL receptor YWTD-containing repeat homology <YW39>
F:3291-3337/Domain: EGF homology <EG13>
F:3331-3366/Domain: LDL receptor ligand-binding repeat homology <LDL>
F:3371-3405/Domain: LDL receptor ligand-binding repeat homology <LDLM>
F:3410-3445/Domain: LDL receptor ligand-binding repeat homology <LDLN>
F:3450-3486/Domain: LDL receptor ligand-binding repeat homology <LDLO>
F:3491-3528/Domain: LDL receptor ligand-binding repeat homology <LDLP>
F:3533-3567/Domain: LDL receptor ligand-binding repeat homology <LDLQ>
F:3572-3606/Domain: LDL receptor ligand-binding repeat homology <LDLR>
F:3610-3644/Domain: LDL receptor ligand-binding repeat homology <LDLS>
F:3651-3687/Domain: LDL receptor ligand-binding repeat homology <LDLT>
F:3692-3728/Domain: LDL receptor ligand-binding repeat homology <LDLV>
F:3738-3774/Domain: LDL receptor ligand-binding repeat homology <LDLV>
F:3783-3820/Domain: EGF homology <EG14>
F:3826-3858/Domain: EGF homology <EG15>
F:3866-3899/Domain: LDL receptor YWTD-containing repeat homology <YW40>
F:3910-3968/Domain: LDL receptor YWTD-containing repeat homology <YW41>
F:3943-4011/Domain: alpha-2-macroglobulin receptor 85k chain #status predicted <85k>
F:3943-4011/Domain: 85k chain extracellular #status predicted <EXT>
F:3969-4011/Domain: LDL receptor YWTD-containing repeat homology <YW42>
F:4012-4055/Domain: LDL receptor YWTD-containing repeat homology <YW43>
F:4056-4098/Domain: LDL receptor YWTD-containing repeat homology <YW44>
F:4099-4141/Domain: LDL receptor YWTD-containing repeat homology <YW45>
F:4150-4181/Domain: EGF homology <EG16>
F:4199-4230/Domain: EGF homology <EG17>
F:4235-4266/Domain: EGF homology <EG18>
F:4271-4302/Domain: EGF homology <EG19>
F:4307-4338/Domain: EGF homology <EG20>
F:4343-4373/Domain: EGF homology <EG21>
F:4376-4408/Domain: EGF homology <EG22>
F:4421-4443/Domain: transmembrane #status predicted <TM>
F:4444-4543/Domain: intracellular #status predicted <INT>
F:116-138,187,276,359,448,731,926,1048,1152,1153,1193,1305,1509,1556,1573,1614,1643,3485,3659,3786,3837,3952,4074,4124,4178,4278/Binding site: carboxyrate (asn) (covalent)
F:168/2995/Modified site: erythro-beta-hydroxyaspartagine (asn) #status predicted
F:2955/Modified site: erythro-beta-hydroxyaspartic acid (asp) #status predicted

Query Match 12.1%; Score 82.5; DB 1; Length 4543;
Best Local Similarity 32.4%; Pred. No. 34;
Matches 24; Conservative 4; Mismatches 23; Indels 23; Gaps 4;

QY 19 GVKDC-----VFCEL-----TDSMQCPGYM-----HCGDEDCFTGHGVAFGTGY 61
DB 2753 GADGCDGSDSDSRCLTTCSTGSGFCGPGTYVCVPRMLCDGKDC-----ADGADETL 2806
QY 62 NKGLRATSCGLEE 75
DB 2807 AAGCLYNTCTDERE 2820

RESULT 8
B41643
urokinase-type plasminogen activator receptor 2 - mouse
C:Species: Mus musculus (house mouse)

C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #ext_change 09-Jul-2004
C:Accession: B41643
R:Kristensen, P.; Eriksen, J.; Blasj, F.; Dano, K.
J. Cell Biol. 115, 1763-1771, 1991
A:Title: Two alternatively spliced mouse urokinase receptor mRNAs with different histologic
A:Reference number: A41643; MUID:92098587; PMID:161735
A:Accession: B41643
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-222 <KRI>
A:Cross-references: UNIPROT:P35457; GB:X62701; NID:g53277; PID:CA44575.1; PID:g53278
F:24-108/Domain: Ly-6 homology <LY6>

Query Match 11.8%; Score 80.5; DB 2; Length 222;
Best Local Similarity 28.7%; Pred. No. 4.1;
Matches 31; Conservative 10; Mismatches 42; Indels 25; Gaps 5;

QY 3 LCMILLVWALPPGTGVNDVCFCELTDSMQCPGYTMHCGDDEDCFTGHGVAFGT----- 58
DB 7 LLLILLATTCVPASGGLQ-CMQCESNQCCLV-----EECALGDLCRTTVLREW 55
QY 59 -----PVINKGCLRATSCGLEEPVSYR--GVYSLTTNCTGRLCNR 98
DB 56 QDDRELEVTVRGCAHSEKTRMTSYRMGSMITLFTVCATNLNR 101

RESULT 9
B55356
urokinase-type plasminogen activator receptor, hypothetical soluble form precursor - mou
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #ext_change 09-Jul-2004
C:Accession: B55356
R:Sub, T.T.; Nerlov, C.; Dano, K.; Degen, J.L.
J. Biol. Chem. 269, 25992-25998, 1994
A:Title: The murine urokinase-type plasminogen activator receptor gene.
A:Reference number: A55356; MUID:95014420; PMID:7829309
A:Accession: B55356
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-222 <SUH>
A:Cross-references: UNIPROT:Q91Z14; GB:U12235
A:Note: authors translated the codon TTG for residue 219 as Phe
C:Genetics:
A:Introns: 20/1; 57/1; 105/1
C:Keywords: alternative splicing; duplication
F:24-108/Domain: Ly-6 homology <LY6>

Query Match 11.8%; Score 80.5; DB 2; Length 222;
Best Local Similarity 28.7%; Pred. No. 4.1;
Matches 31; Conservative 10; Mismatches 42; Indels 25; Gaps 5;

QY 3 LCMILLVWALPPGTGVNDVCFCELTDSMQCPGYTMHCGDDEDCFTGHGVAFGT----- 58
DB 7 LLLILLATTCVPASGGLQ-CMQCESNQCCLV-----EECALGDLCRTTVLREW 55
QY 59 -----PVINKGCLRATSCGLEEPVSYR--GVYSLTTNCTGRLCNR 98
DB 56 QDDRELEVTVRGCAHSEKTRMTSYRMGSMITLFTVCATNLNR 101

RESULT 10
A55356
urokinase-type plasminogen activator receptor membrane form precursor - mouse
N:Alternate names: urokinase-type plasminogen activator receptor 1
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #ext_change 09-Jul-2004
C:Accession: A55356; A41643
R:Sub, T.T.; Nerlov, C.; Dano, K.; Degen, J.L.
J. Biol. Chem. 269, 25992-25998, 1994
A:Title: The murine urokinase-type plasminogen activator receptor gene.
A:Reference number: A55356; MUID:95014420; PMID:7929309
A:Accession: A55356
A:Molecule type: DNA

6 LLLVMAIPPGTTGVKDCVFCELTDSMQCPGTVMHCGDEDCFTGHGVAPGT----- 57

Db 818 STGAVC--CTNTNVIRCPGSSVBEYGGRLACPGASNKKCPQGYSCMPSTNPQHLLCCS 875

Qy 67 RATSGLKEPVSYRGVY-----SLTTCCTGRLCNRA--PSSQTVGAT 108

Db 876 SSGMGVSQPCCLRGVAVNPATNQRFCSPMKADCPAGYTCFESDQSSQFICCT 930

Search completed: April 15, 2005, 14:04:25
Job time : 17 secs

RESULT 14

T27283
hypothetical protein Y64G10A.f - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27283
R:Ainscough, R.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z20336
A:Accession: T27283
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1620 <MIL>
A:Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CA854471.1; CESP:Y64G10A.f
A:Experimental source: clone Y64G10A
C:Genetics:
A:Gene: CESP:Y64G10A.f
A:introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 7

Query Match

11.5%; Score 78.5; DB 2; Length 1620;

Best Local Similarity 29.5%; Pred. No. 33;
Matches 31; Conservative 5; Mismatches 32; Indels 37; Gaps 8;

QY 12 ALPPTGTVKDC-VFCELTDSMOC-----PCTYMH-CGDEDCFTGHGVAPGTGP 59

DB 999 ACAFGTFG-XDCSKKCDADGMHCPSDGRICPPGKGHKC--DETCDSG----- 1046

QY 60 VIKGCLRATSCGLEBPVSRYGVYSLTNNCC-----TGRLCNR 98

DB 1047 LFGAGCKGICSC-----QNGATCDSVTGSCGCRPGMRGKCDR 1084

RESULT 15

S42152

urinary plasminogen activator receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S42152; S41085

R/Rabhani, S.A.; Rajwans, N.; Achbarou, A.; Murthy, K.K.; Goltzman, D.

FEBS Lett. 338, 69-74, 1994

A:Title: Isolation and characterization of multiple isoforms of the rat urokinase recept

A:Reference number: S41085; MUID:94139899; PMID:8307160

A:Accession: S42152

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-328 <RAB>

A:Cross-references: UNIPROT:P49616; EMBL:X71899; NID:9452782; PIDN:CA50718.1; PID:94527

A:Accession: S41085

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-94, 'C', '96-328 <RA2>

A:Cross-references: EMBL:X71898

C:Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

F;118-206/Domain: Ly-6 homology <LY6>

Query Match 11.4%; Score 78; DB 2; Length 328;

Best Local Similarity 24.6%; Pred. No. 9.5;
Matches 30; Conservative 14; Mismatches 70; Indels 8; Gaps 4;

QY 7 LLLVMAIPGTTGVKDCVFCELTDSMOC---PCTYMH-C-GDEDCFTGHGV-APGTGPVI 61

DB 203 VLDLQSLPPNGF--QCYSCEGNSFTGCSYEBSFIDCRGPMNQCLEATGLDVLGNRSYT 259

QY 62 NKGCLRATSCGLEBPVSRYGVYSLTNNCCGRLCNRAPSSQTVGATTSIALGIMLLPP 121

DB 260 VRGCAATASMCQSGHVADSFQTHVNLSTSCNGSGCNRPTGAPGPGPAHLITLTL 319

QY 122 RL 123

DB 320 RL 321